

2.Duffy

AUG 15 2001

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/489,850

DATE: 08/08/2001
TIME: 16:14:04
TECH CENTER 1600/2900

Input Set : N:\Crf3\RULE60\09489850.txt
Output Set: N:\CRF3\08082001\I489850.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: VAN ALSTYNE, Diane
7 SHARMA, Lawrence Rajendra
9 (ii) TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
10 BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
11 CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
13 (iii) NUMBER OF SEQUENCES: 75
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Foley & Lardner
17 (B) STREET: 3000 K Street, N.W., Suite 500
18 (C) CITY: Washington
19 (D) STATE: D.C.
20 (E) COUNTRY: USA
21 (F) ZIP: 20007-5109
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/489,850
C--> 31 (B) FILING DATE: 24-Jan-2000
32 (C) CLASSIFICATION:
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/988,444
36 (B) FILING DATE:
38 (A) APPLICATION NUMBER: US 08/127,499
39 (B) FILING DATE: 28-SEP-1993
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: BENT, Stephen A.
43 (B) REGISTRATION NUMBER: 29,768
44 (C) REFERENCE/DOCKET NUMBER: 51916/103/INBI
46 (ix) TELECOMMUNICATION INFORMATION:
47 (A) TELEPHONE: (202)672-5300
48 (B) TELEFAX: (202)672-5399
49 (C) TELEX: 904136
52 (2) INFORMATION FOR SEQ ID NO: 1:
54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 992 amino acids
56 (B) TYPE: amino acid
57 (C) STRANDEDNESS:
58 (D) TOPOLOGY: unknown
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66 Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu
67 1 5 10 15
69 Glu Ala Gln Ser Arg Ala Leu Arg Ala Gly Leu Ala Ala Gly Ala Ser

ENTERED

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70		20		25		30													
72	Gln	Ser	Arg	Arg	Pro	Arg	Pro	Pro	Arg	His	Ala	Arg	Leu	Gln	His	Leu			
73			35				40						45						
75	Pro	Glu	Met	Thr	Pro	Ala	Val	Thr	Pro	Glu	Gly	Pro	Ala	Pro	Pro	Arg			
76			50				55					60							
78	Thr	Gly	Ala	Trp	Gln	Arg	Lys	Asp	Trp	Ser	Arg	Ala	Pro	Pro	Pro	Pro			
79	65					70				75						80			
81	Glu	Glu	Arg	Gln	Glu	Ser	Arg	Ser	Gln	Thr	Pro	Ala	Pro	Lys	Pro	Ser			
82				85						90					95				
84	Arg	Ala	Pro	Pro	Gln	Gln	Pro	Gln	Pro	Pro	Arg	Met	Gln	Thr	Gly	Arg			
85			100						105					110					
87	Gly	Gly	Ser	Ala	Pro	Arg	Pro	Glu	Leu	Gly	Pro	Pro	Thr	Asn	Pro	Phe			
88			115				120						125						
90	Gln	Ala	Ala	Val	Ala	Arg	Gly	Leu	Arg	Pro	Pro	Leu	His	Asp	Pro	Asp			
91		130				135					140								
93	Thr	Glu	Ala	Pro	Thr	Glu	Ala	Cys	Val	Thr	Ser	Trp	Leu	Trp	Ser	Glu			
94	145				150					155						160			
96	Gly	Glu	Gly	Ala	Val	Phe	Tyr	Arg	Val	Asp	Leu	His	Phe	Ile	Asn	Leu			
97			165						170						175				
99	Gly	Thr	Pro	Pro	Leu	Asp	Glu	Asp	Gly	Arg	Trp	Asp	Pro	Ala	Leu	Met			
100			180						185				190						
102	Tyr	Asn	Pro	Cys	Gly	Pro	Glu	Pro	Pro	Ala	His	Val	Val	Arg	Ala	Tyr			
103			195					200					205						
105	Asn	Gln	Pro	Ala	Gly	Asp	Val	Arg	Gly	Val	Trp	Gly	Lys	Gly	Glu	Arg			
106		210				215						220							
108	Thr	Tyr	Ala	Glu	Gln	Asp	Phe	Arg	Val	Gly	Gly	Thr	Arg	Trp	His	Arg			
109	225				230					235						240			
111	Leu	Leu	Arg	Met	Pro	Val	Arg	Gly	Leu	Asp	Gly	Asp	Thr	Ala	Pro	Leu			
112			245						250						255				
114	Pro	Pro	His	Thr	Glu	Arg	Ile	Glu	Thr	Arg	Ser	Ala	Arg	His	Pro				
115			260					265					270						
117	Trp	Arg	Ile	Arg	Phe	Gly	Ala	Pro	Gln	Ala	Phe	Leu	Ala	Gly	Leu	Leu			
118		275				280						285							
120	Leu	Ala	Ala	Val	Ala	Val	Gly	Thr	Ala	Arg	Ala	Gly	Leu	Gln	Pro	Arg			
121		290				295						300							
123	Ala	Asp	Met	Ala	Ala	Pro	Pro	Met	Pro	Pro	Gln	Pro	Pro	Arg	Ala	His			
124	305				310					315						320			
126	Gly	Gln	His	Tyr	Gly	His	His	His	His	Gln	Leu	Pro	Phe	Leu	Gly	His			
127			325							330					335				
129	Asp	Gly	His	His	Gly	Gly	Thr	Leu	Arg	Val	Gly	Gln	His	His	Arg	Asn			
130			340					345					350						
132	Ala	Ser	Asp	Val	Leu	Pro	Gly	His	Trp	Leu	Gln	Gly	Gly	Trp	Gly	Cys			
133		355					360					365							
135	Tyr	Asn	Leu	Ser	Asp	Trp	His	Gln	Gly	Thr	His	Val	Cys	His	Thr	Lys			
136		370				375						380							
138	His	Met	Asp	Phe	Trp	Cys	Val	Glu	His	Asp	Arg	Pro	Pro	Pro	Ala	Thr			
139	385				390					395						400			
141	Pro	Thr	Ser	Leu	Thr	Ala	Ala	Asn	Tyr	Ile	Ala	Ala	Ala	Ala	Thr	Pro			
142				405					410						415				

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144   Ala Thr Ala Pro Pro Pro Cys His Ala Gly Leu Asn Asp Ser Cys Gly
145           420                     425                     430
147   Gly Phe Leu Ser Gly Cys Gly Pro Met Arg Leu Pro Thr Ala Leu Thr
148           435                     440                     445
150   Pro Gly Ala Val Gly Asp Leu Arg Ala Val His His Arg Pro Val Pro
151           450                     455                     460
153   Ala Tyr Pro Val Cys Cys Ala Met Arg Trp Gly Leu Pro Pro Trp Glu
154   465                     470                     475                     480
156   Leu Val Ile Leu Thr Ala Arg Pro Glu Asp Gly Trp Thr Cys Arg Gly
157           485                     490                     495
159   Val Pro Ala His Pro Gly Thr Arg Cys Pro Glu Leu Val Ser Pro Met
160           500                     505                     510
162   Gly Arg Ala Thr Cys Ser Pro Ala Ser Ala Leu Trp Leu Ala Thr Ala
163           515                     520                     525
165   Asn Ala Leu Ser Leu Asp His Ala Phe Ala Ala Phe Val Leu Leu Val
166   530                     535                     540
168   Pro Trp Val Leu Ile Phe Met Val Cys Arg Arg Ala Cys Arg Arg Pro
169   545                     550                     555                     560
171   Ala Pro Pro Pro Pro Ser Pro Gln Ser Ser Cys Arg Gly Thr Thr Pro
172           565                     570                     575
174   Pro Ala Tyr Gly Glu Glu Ala Phe Thr Tyr Leu Cys Thr Ala Pro Gly
175           580                     585                     590
177   Cys Ala Thr Gln Thr Pro Val Pro Val Arg Leu Ala Gly Val Gly Phe
178           595                     600                     605
180   Glu Ser Lys Ile Val Asp Gly Gly Cys Phe Ala Pro Trp Asp Leu Glu
181   610                     615                     620
183   Ala Thr Gly Ala Cys Ile Cys Glu Ile Pro Thr Asp Val Ser Cys Glu
184   625                     630                     635                     640
186   Gly Leu Gly Ala Trp Val Pro Thr Ala Pro Cys Ala Arg Ile Trp Asn
187           645                     650                     655
189   Gly Thr Gln Arg Ala Cys Thr Phe Trp Ala Val Asn Ala Tyr Ser Ser
190           660                     665                     670
192   Gly Gly Tyr Ala Gln Leu Ala Ser Tyr Phe Asn Pro Gly Gly Ser Tyr
193           675                     680                     685
195   Tyr Lys Gln Tyr His Pro Thr Ala Cys Glu Val Glu Pro Ala Phe Gly
196   690                     695                     700
198   His Ser Asp Ala Ala Cys Trp Gly Phe Pro Thr Asp Thr Val Met Ser
199   705                     710                     715                     720
201   Val Phe Ala Leu Ala Ser Tyr Val Gln His Pro His Lys Thr Val Arg
202           725                     730                     735
204   Val Lys Phe His Thr Glu Thr Arg Thr Val Trp Gln Leu Ser Val Ala
205           740                     745                     750
207   Gly Val Ser Cys Asn Val Thr Thr Glu His Pro Phe Cys Asn Thr Pro
208           755                     760                     765
210   His Gly Gln Leu Glu Val Gln Val Pro Pro Asp Pro Gly Asp Leu Val
211   770                     775                     780
213   Glu Tyr Ile Met Asn Tyr Thr Gly Asn Gln Gln Ser Arg Trp Gly Leu
214   785                     790                     795                     800
216   Gly Ser Pro Asn Cys His Gly Pro Asp Trp Ala Ser Pro Val Cys Gln

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217					805					810					815	
219	Arg	His	Ser	Pro	Asp	Cys	Ser	Arg	Leu	Val	Gly	Ala	Thr	Pro	Glu	Arg
220					820					825					830	
222	Pro	Arg	Leu	Arg	Leu	Val	Asp	Ala	Asp	Asp	Pro	Leu	Leu	Arg	Thr	Ala
223					835					840					845	
225	Pro	Gly	Pro	Gly	Glu	Val	Trp	Val	Thr	Pro	Val	Ile	Gly	Ser	Gln	Ala
226					850					855					860	
228	Arg	Lys	Cys	Gly	Leu	His	Ile	Arg	Ala	Gly	Pro	Tyr	Gly	His	Ala	Thr
229					865					870					875	880
231	Val	Glu	Met	Pro	Glu	Trp	Ile	His	Ala	His	Thr	Thr	Ser	Asp	Pro	Trp
232					885					890					895	
234	His	Pro	Pro	Gly	Pro	Leu	Gly	Leu	Lys	Phe	Lys	Thr	Val	Arg	Pro	Val
235					900					905					910	
237	Ala	Leu	Pro	Arg	Ala	Leu	Ala	Pro	Pro	Arg	Asn	Val	Arg	Val	Thr	Gly
238					915					920					925	
240	Cys	Tyr	Gln	Cys	Gly	Thr	Pro	Ala	Leu	Val	Glu	Gly	Leu	Ala	Pro	Gly
241					930					935					940	
243	Gly	Gly	Asn	Cys	His	Leu	Thr	Val	Asn	Gly	Glu	Asp	Val	Gly	Ala	Phe
244					945					950					955	960
246	Pro	Pro	Gly	Lys	Phe	Val	Thr	Ala	Ala	Leu	Leu	Asn	Thr	Pro	Pro	Pro
247					965					970					975	
249	Tyr	Gln	Val	Ser	Cys	Gly	Gly	Glu	Ser	Asp	Arg	Ala	Ser	Ala	Gly	His
250					980					985					990	

253 (2) INFORMATION FOR SEQ ID NO: 2:

255 (i) SEQUENCE CHARACTERISTICS:

256 (A) LENGTH: 21 amino acids

257 (B) TYPE: amino acid

258 (C) STRANDEDNESS:

259 (D) TOPOLOGY: unknown

265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

267 Pro Ser Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr

268 1 5 10 15

270 Gly Arg Gly Gly Ser

271 20

273 (2) INFORMATION FOR SEQ ID NO: 3:

275 (i) SEQUENCE CHARACTERISTICS:

276 (A) LENGTH: 7 amino acids

277 (B) TYPE: amino acid

278 (C) STRANDEDNESS:

279 (D) TOPOLOGY: unknown

285 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

287 Gln Pro Gln Pro Pro Arg Met

288 1 5

290 (2) INFORMATION FOR SEQ ID NO: 4:

292 (i) SEQUENCE CHARACTERISTICS:

293 (A) LENGTH: 21 amino acids

294 (B) TYPE: amino acid

295 (C) STRANDEDNESS:

296 (D) TOPOLOGY: unknown

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302 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
304   Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser Arg
305     1           5           10           15
307   Ala Pro Pro Gln Gln
308     20
310 (2) INFORMATION FOR SEQ ID NO: 5:
312 (i) SEQUENCE CHARACTERISTICS:
313 (A) LENGTH: 7 amino acids
314 (B) TYPE: amino acid
315 (C) STRANDEDNESS:
316 (D) TOPOLOGY: unknown
322 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
324   Gln Thr Pro Ala Pro Lys Pro
325     1           5
327 (2) INFORMATION FOR SEQ ID NO: 6:
329 (i) SEQUENCE CHARACTERISTICS:
330 (A) LENGTH: 21 amino acids
331 (B) TYPE: amino acid
332 (C) STRANDEDNESS:
333 (D) TOPOLOGY: unknown
339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
341   Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His Gly
342     1           5           10           15
344   Gln His Tyr Gly His
345     20
347 (2) INFORMATION FOR SEQ ID NO: 7:
349 (i) SEQUENCE CHARACTERISTICS:
350 (A) LENGTH: 7 amino acids
351 (B) TYPE: amino acid
352 (C) STRANDEDNESS:
353 (D) TOPOLOGY: unknown
359 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
361   Pro Pro Gln Pro Pro Arg Ala
362     1           5
364 (2) INFORMATION FOR SEQ ID NO: 8:
366 (i) SEQUENCE CHARACTERISTICS:
367 (A) LENGTH: 1063 amino acids
368 (B) TYPE: amino acid
369 (C) STRANDEDNESS:
370 (D) TOPOLOGY: unknown
376 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
378   Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu
379     1           5           10           15
381   Glu Ala Gln Ser Arg Ala Leu Arg Ala Glu Leu Ala Ala Gly Ala Ser
382           20           25           30
384   Gln Ser Arg Arg Pro Arg Pro Pro Arg Gln Arg Asp Ser Ser Thr Ser
385           35           40           45
387   Gly Asp Asp Ser Gly Arg Asp Ser Gly Gly Pro Arg Arg Arg Gly
388           50           55           60

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/489,850

DATE: 08/08/2001

TIME: 16:14:05

Input Set : N:\Crf3\RULE60\09489850.txt

Output Set: N:\CRF3\08082001\I489850.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:1170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23